

FIG. I

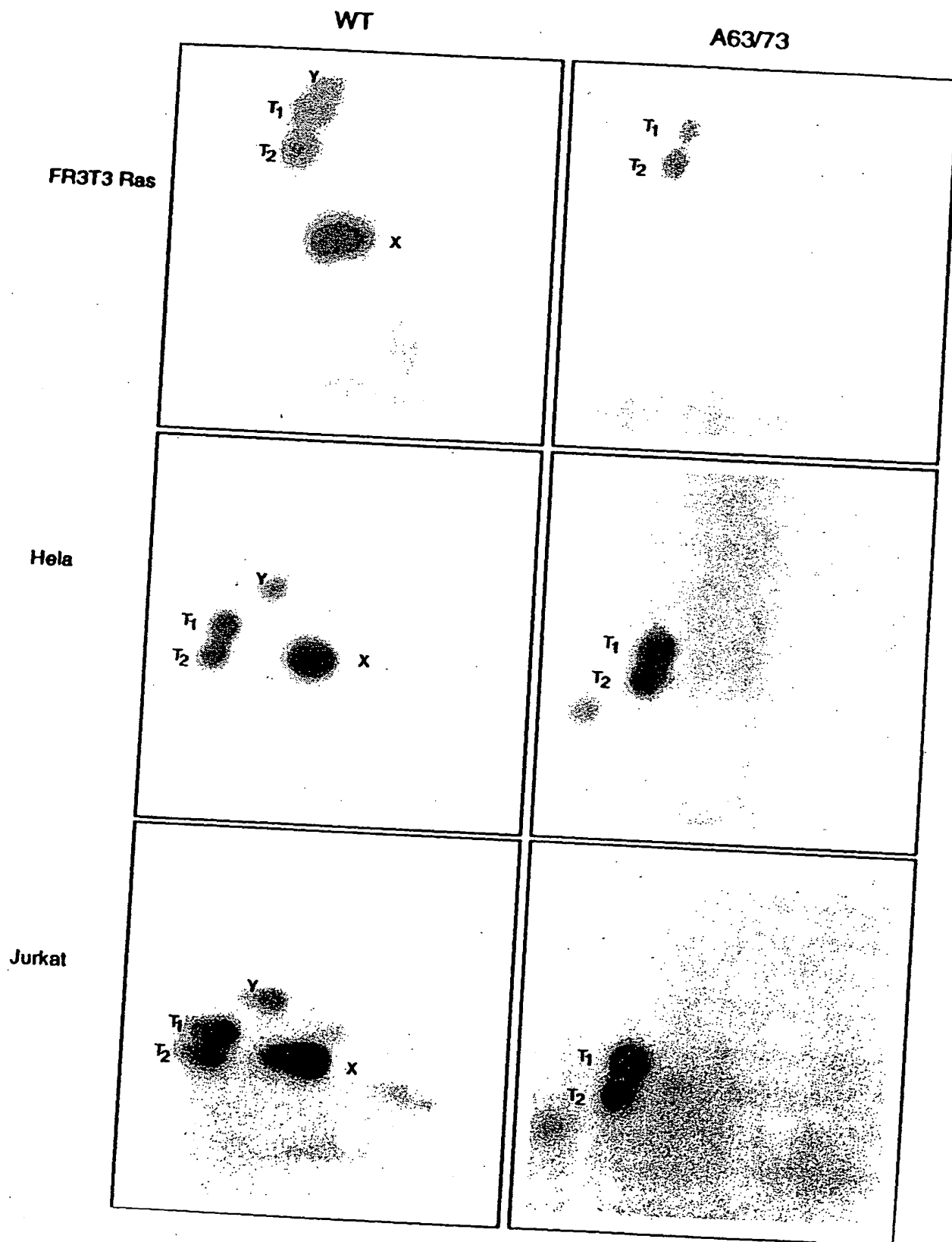


FIG. 3A

In Vitro

In Vivo

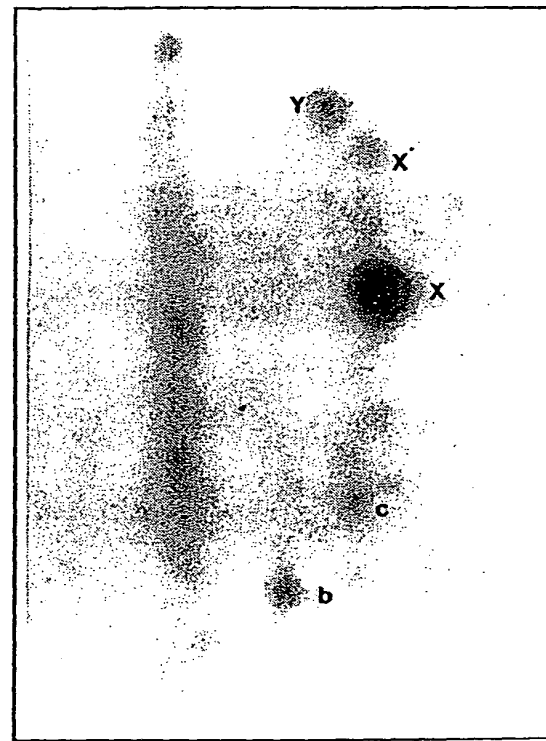
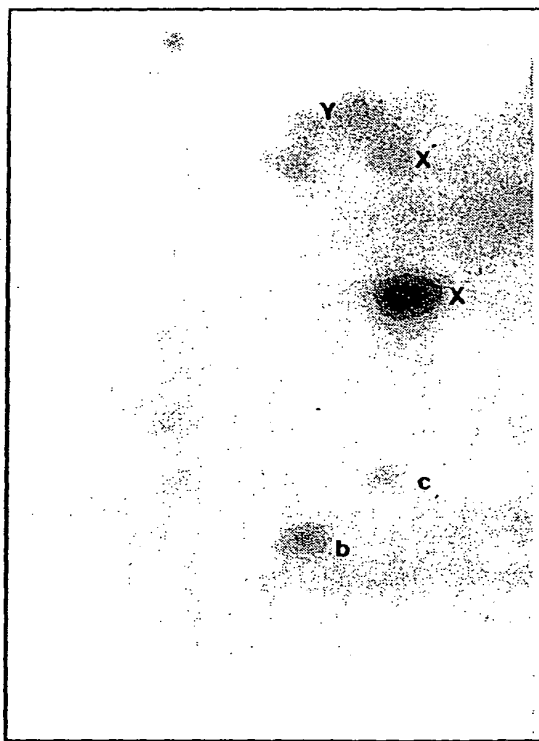


FIG. 3B

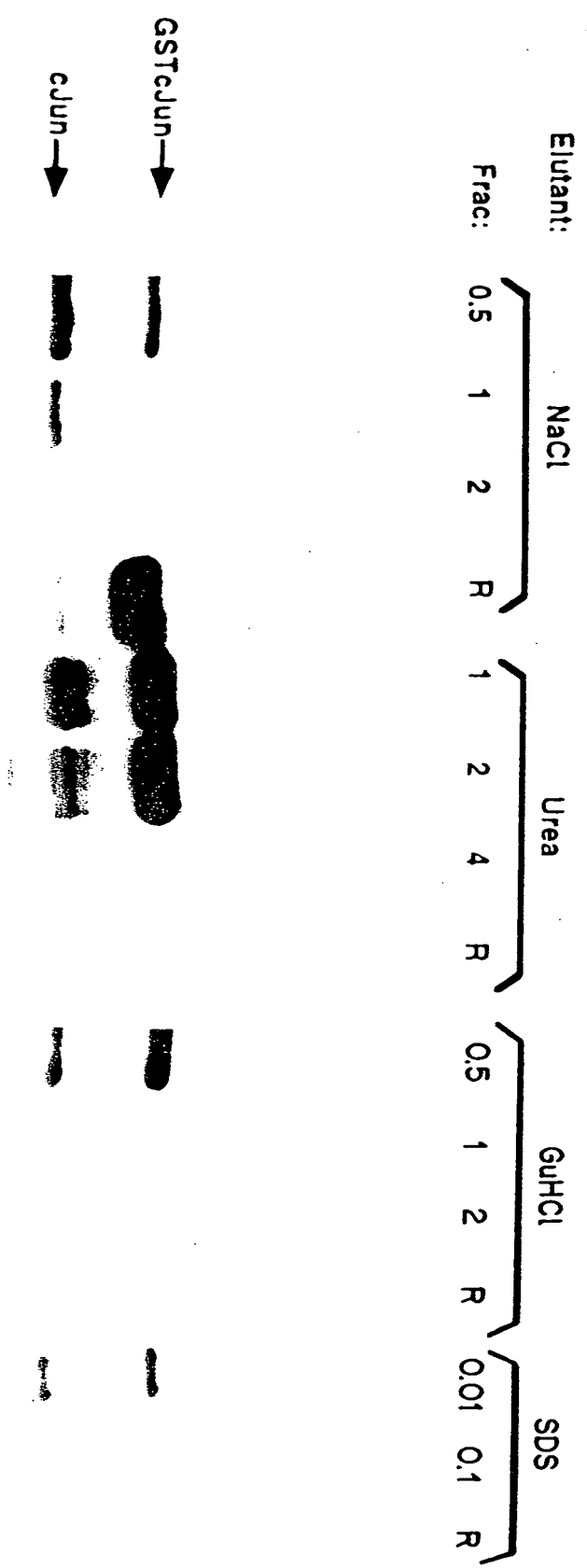


FIG. 4A

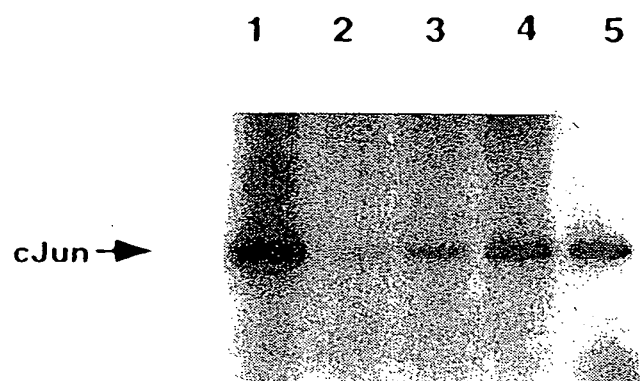


FIG. 4B

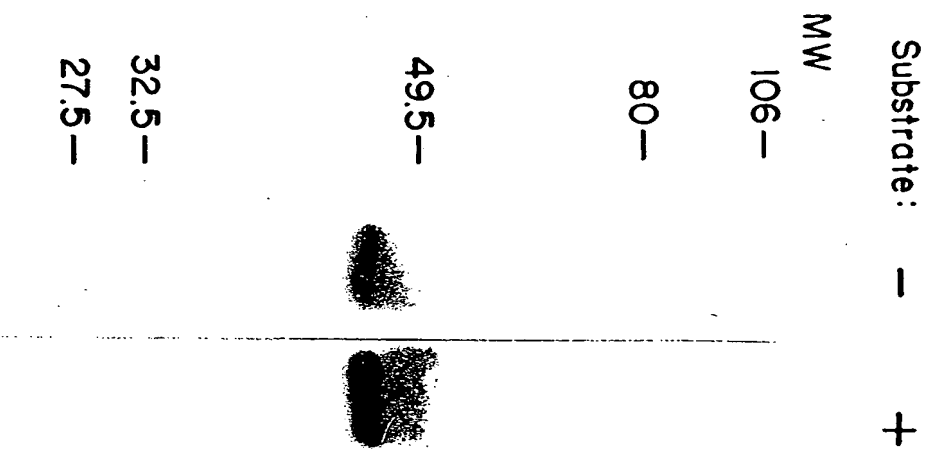


FIG. 5A

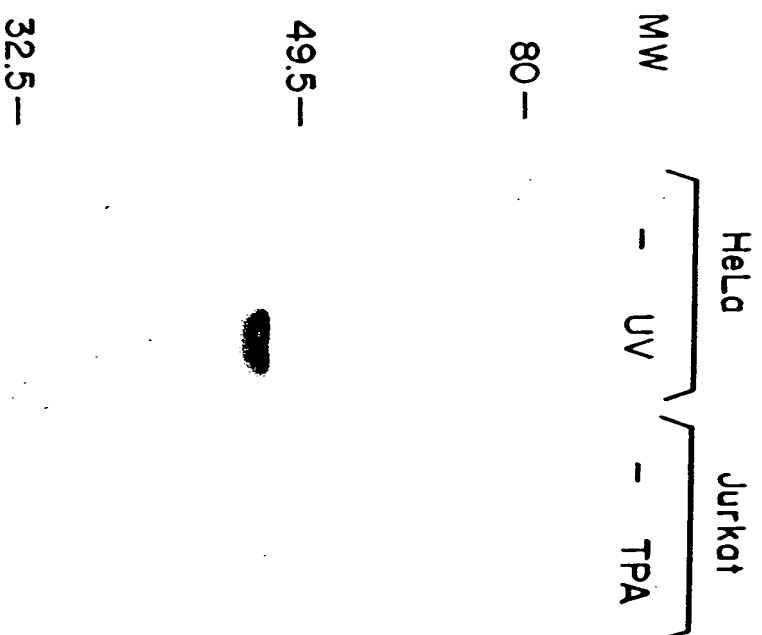


FIG. 5B

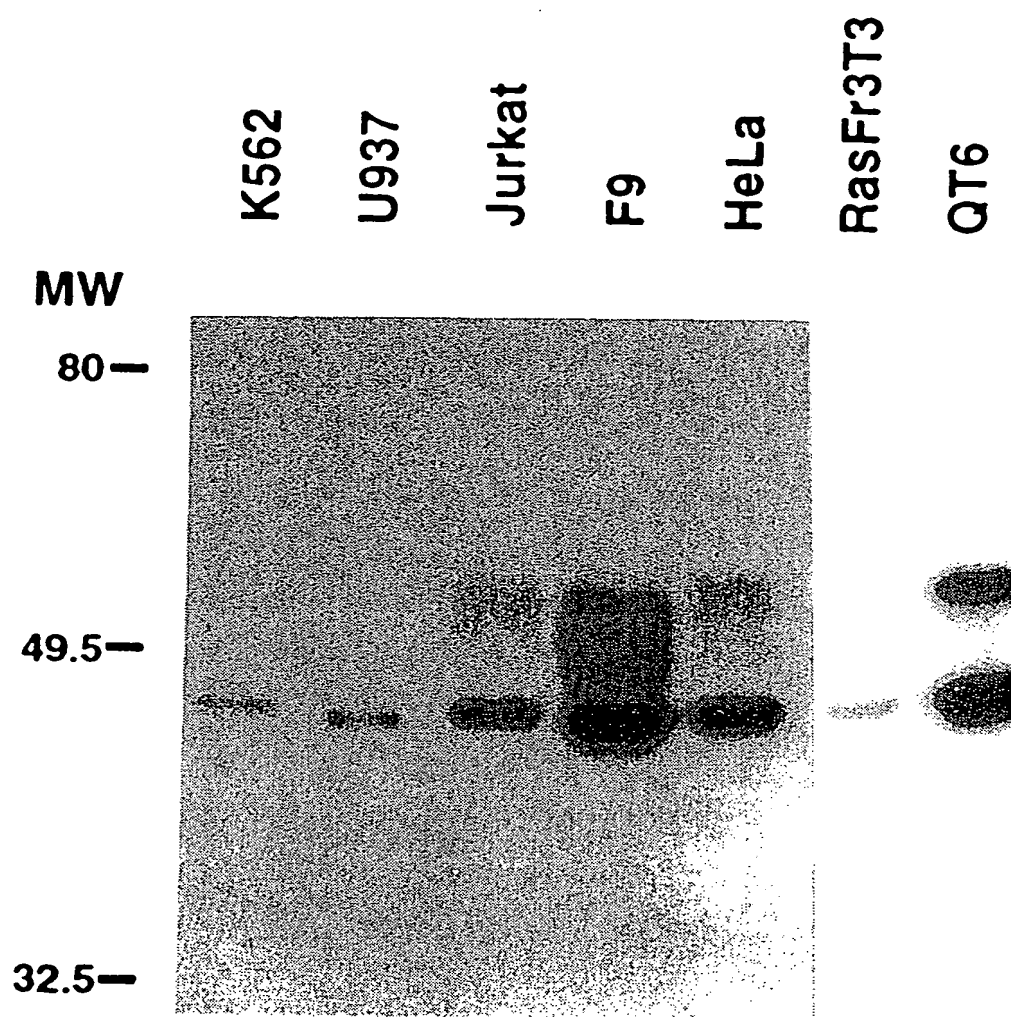
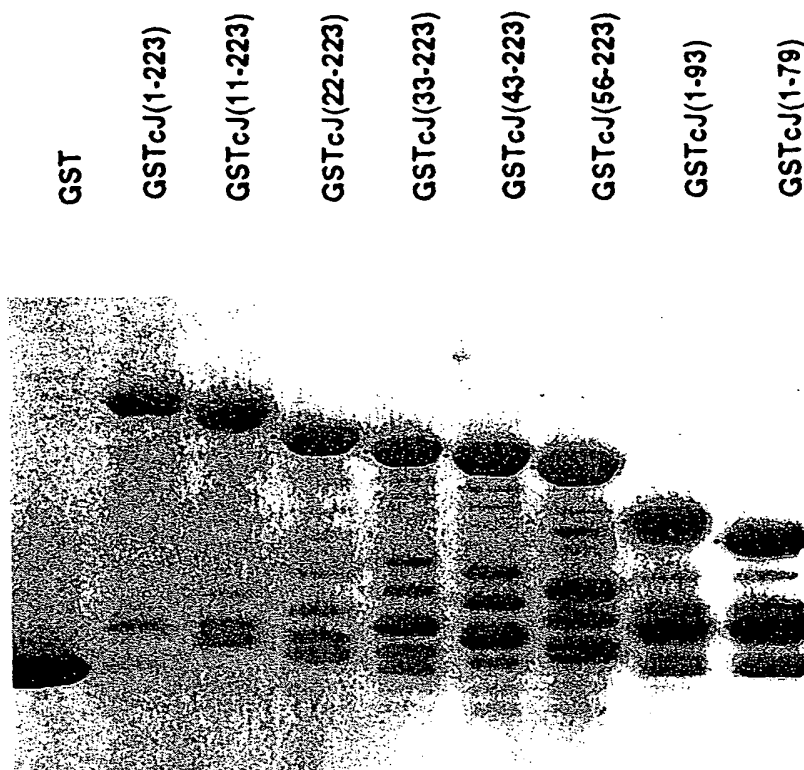


FIG. 5C

Protein Gel

FIG.6A



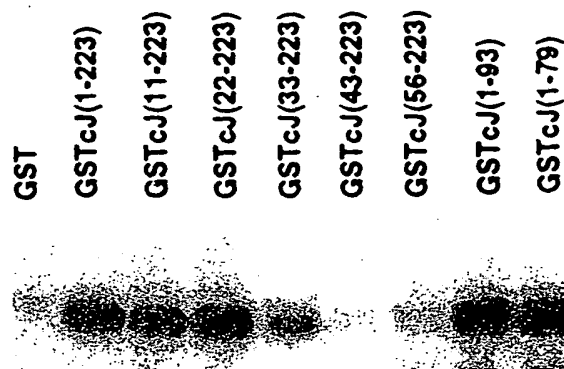
³²P-Immobilized
Substrate

FIG.6B



³²P-Exogenous
Substrate

FIG.6C



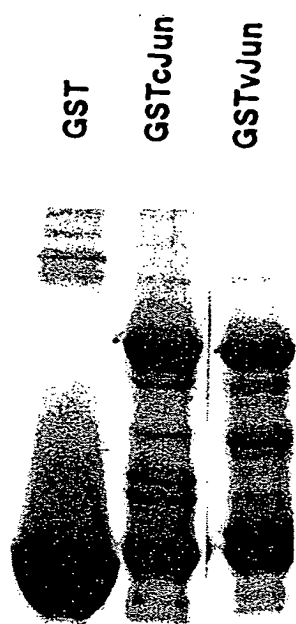


FIG. 7A

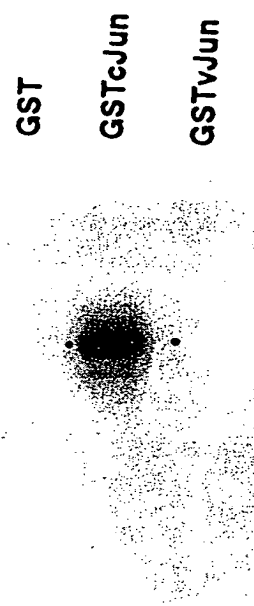


FIG. 7B

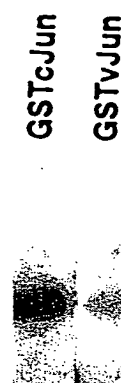


FIG. 7C

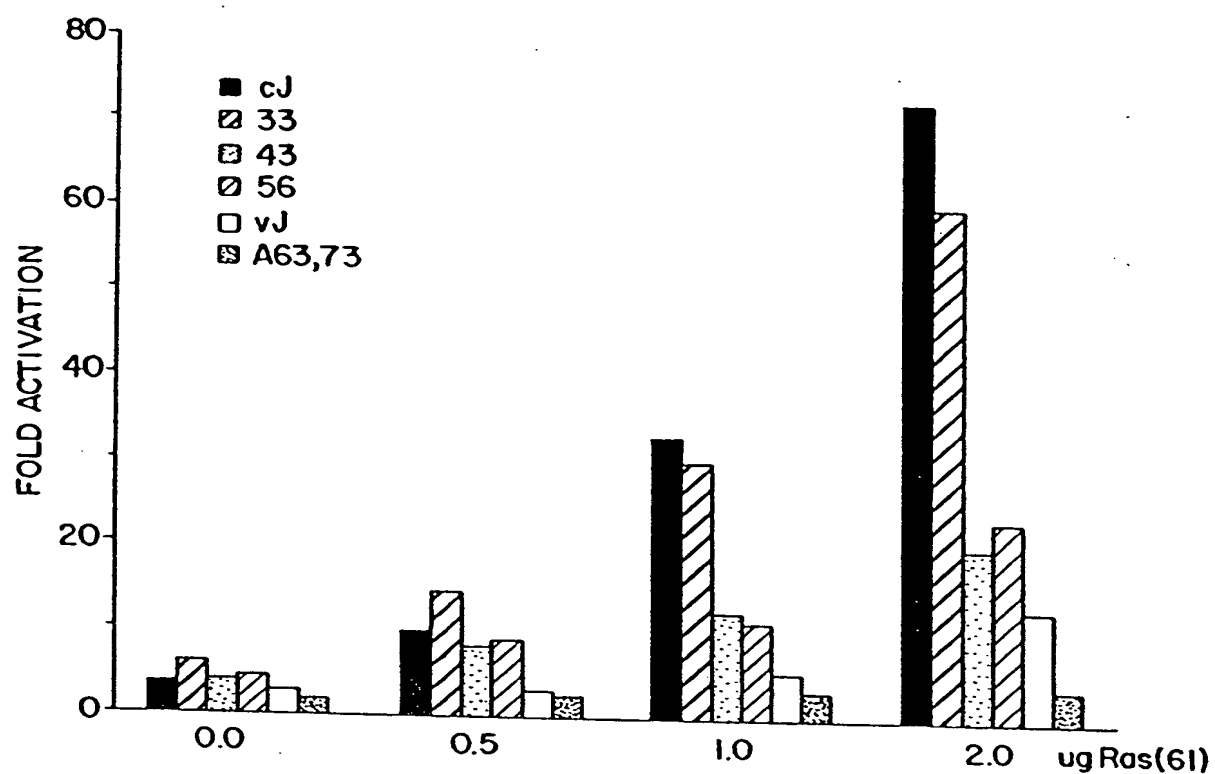


FIG. 8A

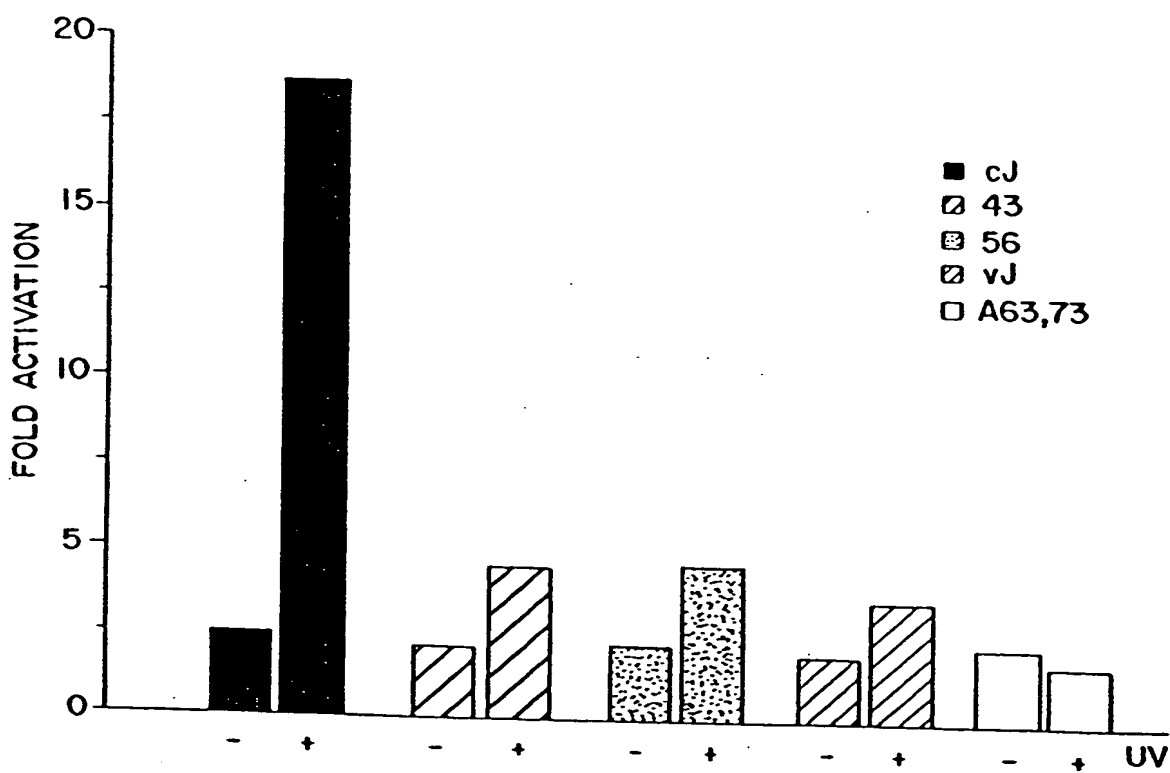


FIG. 8B

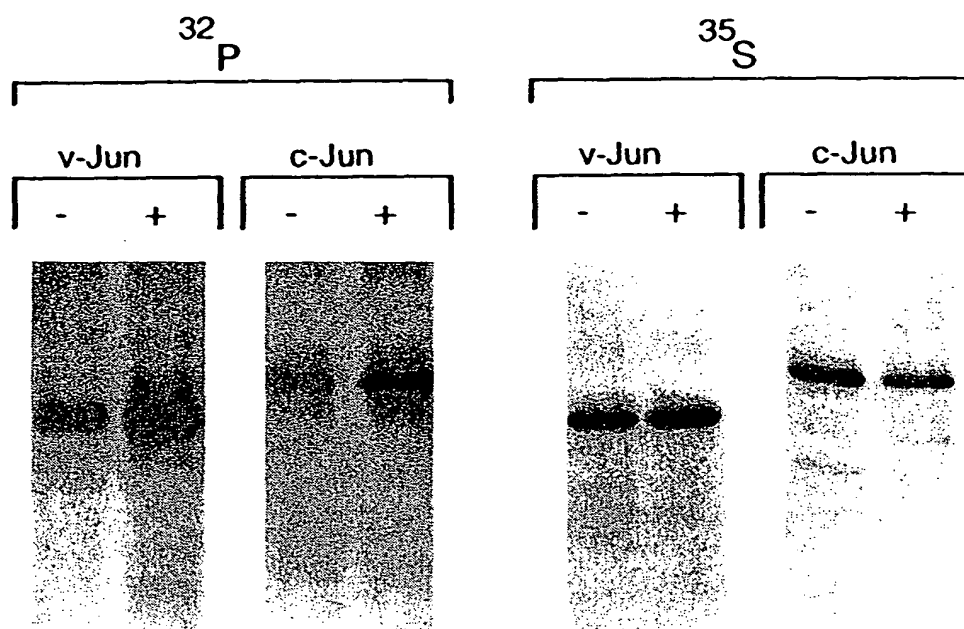


FIG.9A

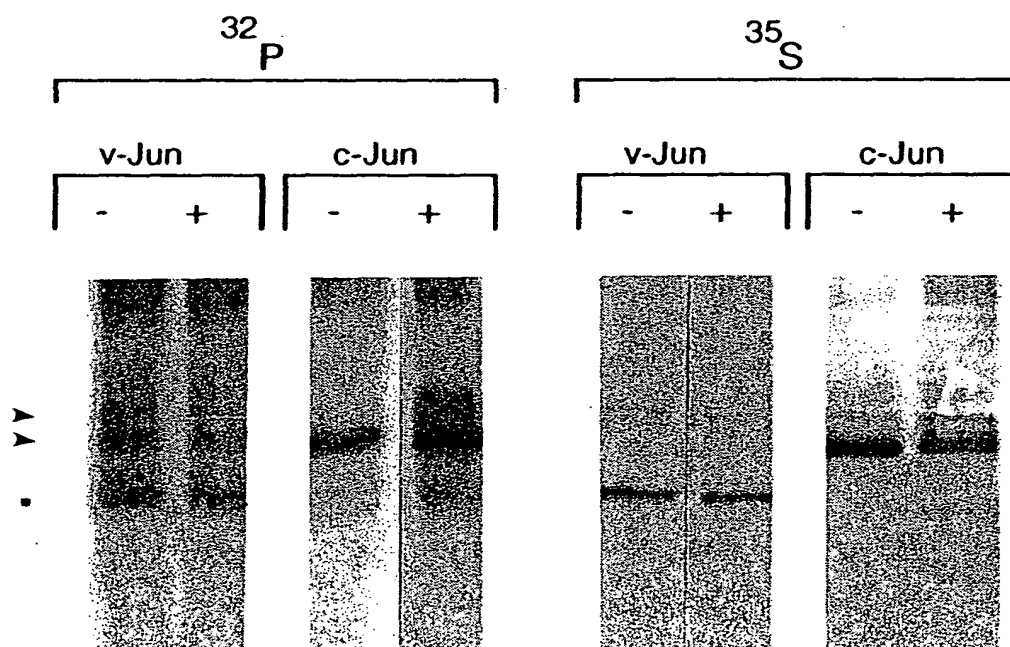


FIG.9B

GAATTCCGGG GCGGCCAAGA CCGCGCGCGG GCGGCCACT GCAGGTCCG CACTGATCCG	60
CTCCGGCGGA GAGCCGCTGC TCTGGGAAGT CAGTTCCCT GCGACTCCG AGGAACCGCT	120
GCGCACCGAAG AGCCGTCAGT GAGTGACCGC GACTTTCAA AGCCGGGTAG GCGCGCGAG	180
TCGACAACTA AGAGTCCGGG AGGCATCTA ATTAACCTG CGCTCCCTCG AGCAGCTGCT	240
GAGGAGGGCG CACGGGGACG ACAGCCAGCG GGTGCGTGG CTCTTAGAGA AACTTCCCT	300
GTCAAAGGCT CCGGGGGCG CGGGTGTCG CCGCTTGCCA CAGCCCTGTT GCGGCCCCGA	360
AACTTGTCG CGCAGGCCAA ACTAACCCTCA CGTGAAGTGA CGGACTGTTC T ATG ACT	417
Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala Ser Phe	465
CTC CCC TCC GAG AGG GGA CCT TAT GGC TAC AGT AAC CCC AAG ATC CTG	513
Leu Pro Ser Glu Arg Gly Pro Tyr Gly Tyr Ser Asn Pro Lys Ile Leu	
AAA CAG AGC ATG ACC CTG AAC CTG GCC GAC CCA GTG GGG AGC CTG AAG	561
Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser Leu Lys	

FIG.10A

CCG CAC CTC CGC GCC AAC AAC TCG GAC CTC CTC ACC TCG CCC GAC GTG	609
Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro Asp Val	
55	60
65	
GGG CTG CTC AAG CTG CGC TCG CCC GAG CTG GAG CGC CTG ATA ATC CAG	657
Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile Ile Gln	
70	75
80	
TCC AGC AAC GCG CAC ATC ACC ACC ACC CCG ACC CCC ACC CAG TTC CTG	705
Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln Phe Leu	
85	90
95	
TGC CCC AAG AAC GTG ACA GAT GAG CAG GAG GCG TTC GCC GAG GCG TTC	753
Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu Gly Phe	
100	105
110	
GTG CGC GCC CTG GCC GAA CTG CAC ACC CAG AAC ACC GCG CTG CCC AGC CTC	801
Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro Ser Val	
115	120
125	
130	
ACG TCG GCG GCG CAG CCG GTC AAC GCG GCA GCG ATG GTG GCT CCC GCG	849
Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala Pro Ala	
135	140
145	
GTA GCC TCG GTG GCA GCG GCG ACC GCG ACC GCG TTC ACC GCG AGC	897
Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser Ala Ser	
150	155
160	

FIG.10B

CTG CAC ACC GAG CCG CCG CTC TAC GCA AAC CTC AGC AAC TTC AAC CCA	945
Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe Asn Pro	
165	
GCC GCC CTG AGC AGC GGC GGC GGC GGC CCC TCC TAC GGC GGC GGC GGC	993
Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala Ala Gly	
180	
CTG GCC TTT CCC GCG CAA CCC CAG CAG CAG CAG CAG CCG CCG CAC CAC	1041
Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Gln Pro Pro His His	
195	
CTG CCC CAG CAG ATG CCC GTG CAG CAC CCG CGG CTG CAG GCC CTG AAG	1089
Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala Leu Lys	
215	
GAG GAG CCT CAG ATA GTG CCC GAG ATG CCC GCG GAG GAG ACA CCG CCC CTG	1137
Glu Glu Pro Gln Ile Val Pro Glu Met Pro Gly Glu Thr Pro Pro Leu	
230	
TCC CCC ATC GAC ATG GAG TCC CAG GAG CCG ATC AAG GCG GAG AGG AAG	1185
Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu Arg Lys	
245	
CGC ATG AGG AAC CCG ATC GCT GCC TCG AAG TGC CGA AAA AGG AAG CTG	1233
Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg Lys Leu	
260	
265	
270	

FIG.10C

GAG AGA ATC GCC CGG CTG GAG GAA AAA GTG AAA ACC TTG AAA GCT CAG	1281
Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln	290
275	
AAC TCG GAG CTG GCG TCG ACG GCC AAC ATG CTC AGG GAA CAG GTC GCA	1329
Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala	305
295	
CAG CTT AAA CAC AAA GTC ATG AAC CAC GTT AAC AGT GCG TGC CAA CTC	1377
Gln Leu Lys His Lys Val Met Asn His Val Asn Ser Gly Cys Gln Leu	320
310	
ATC CTA ACG CAG CAG TTG CAA ACA TTT TGAAGAGAGA CCGTCGGCGC	1424
Ile Leu Thr Gln Gln Leu Gln Thr Phe	330
325	
CTGAGGGGCA ACGAAGAAAA AAAATAACAC AGAGAGACAG ACTTGAGAAC TTGACAAGTT	1484
GGCAGCGAGA GAAAAAAGAA GTGTCCGAGA ACTAAAGCCA AGGCTATCCA AGTTGGACTG	1544
GGTTGGGTCT GACGGCGCCC CCAGTGTGCA CGAGTGGGAA CCACCTGCTC GCGCCCTCCC	1604
TTGGCGTCCA GCCAGGGAGC GCGCCCTGG GCGCTGCCCC GCTTGGCGA CGGCTGTCC	1664
CCCCGGCAAC GGAACGTTGG ACTTTCGTTA ACATTGACCA AGAACTGCAT GGACCTAACA	1724

FIG.10D

TTGATCTCA TTCAGTATTA AAGGGGCAG GGGAGGGG TTACAACCTG CAATAGAGAC	1784
TGTAGATTGC TTCTGTAGTA CTCCTTAAGA ACACAAGCG GGGGAGCGT TGGGAGGGG	1844
CGGCAGGAGC GAGGTTTGTG AGAGCGAGCG TGAGCCTACA GATGAAGCTT TTCTGGCCTG	1904
CTTTCGTTAA CTGTGTATGT ACATATATAT ATTTTAAAT TTGATTAAAG CTGATTACTG	1964
TCAATAAACA GCTTCATGCC TTGTAAGTT ATTTCTTCTT TGTTCCTTG GGATCCTGCC	2024
CAGTGTCTT TGTAAATAAG AGATTGGAG CACTCTGACT TTACCAITTG TAATAAGTA	2084
TATAATTTT TT	2096

FIG.10E

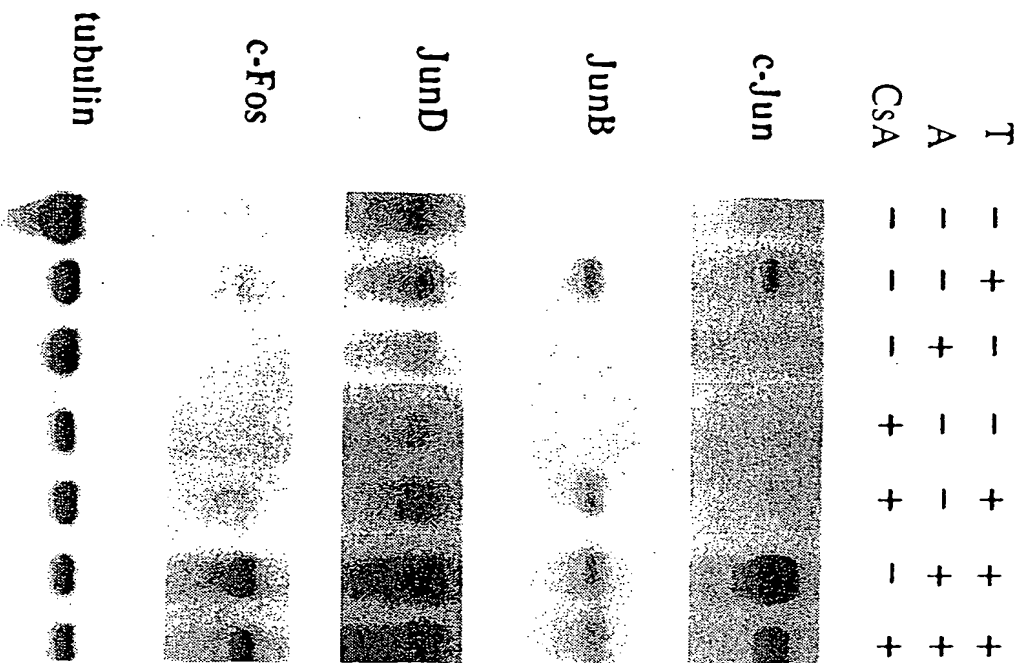


FIG. 11A

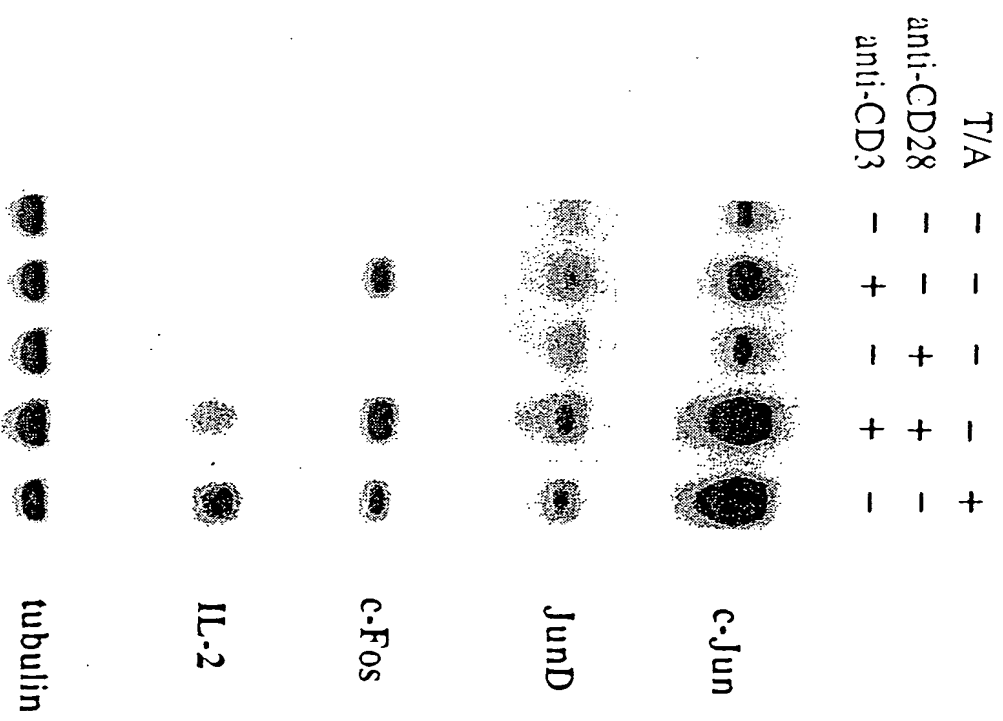


FIG. 11B

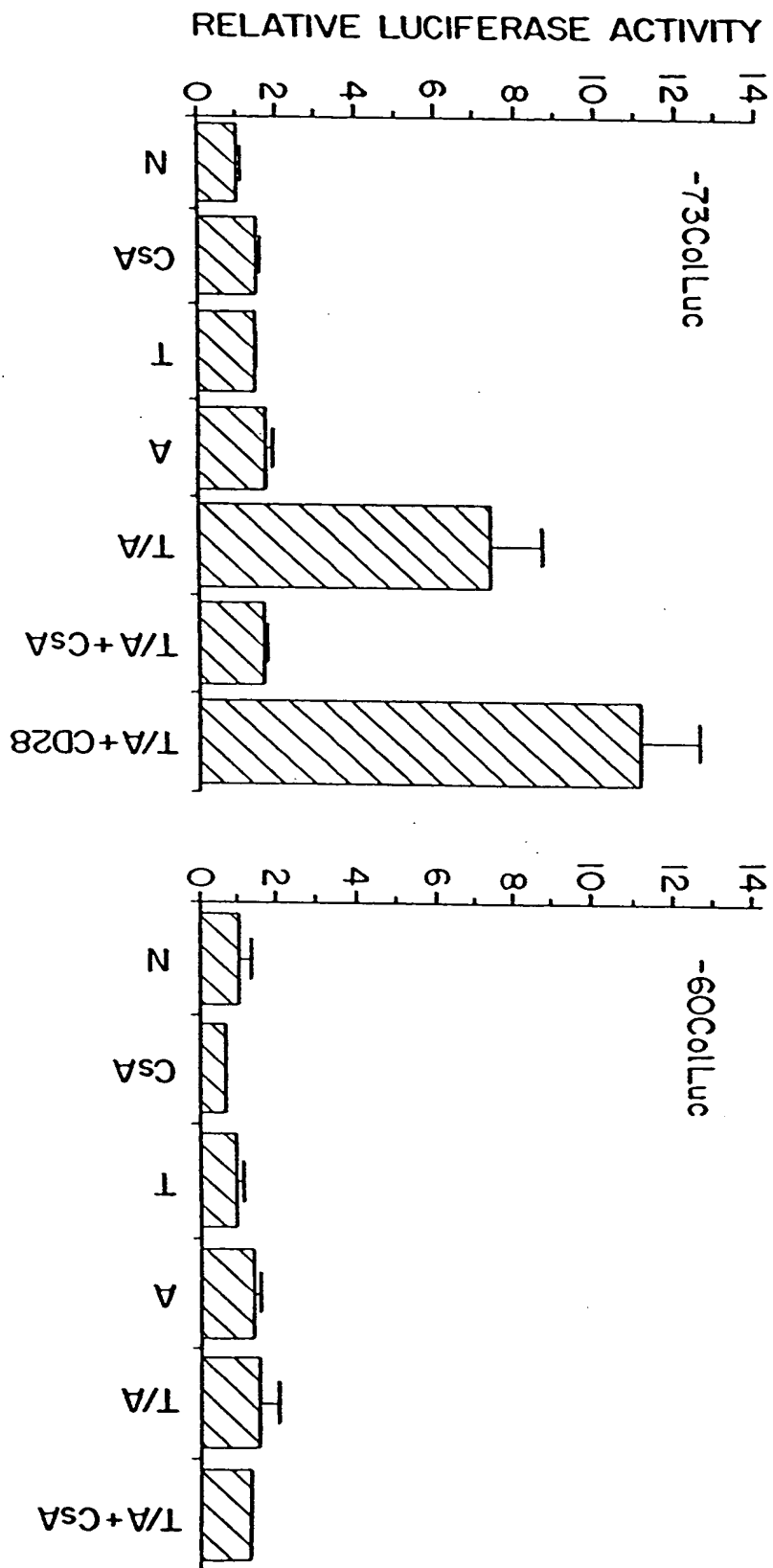


FIG. 11C

FIG. 12A

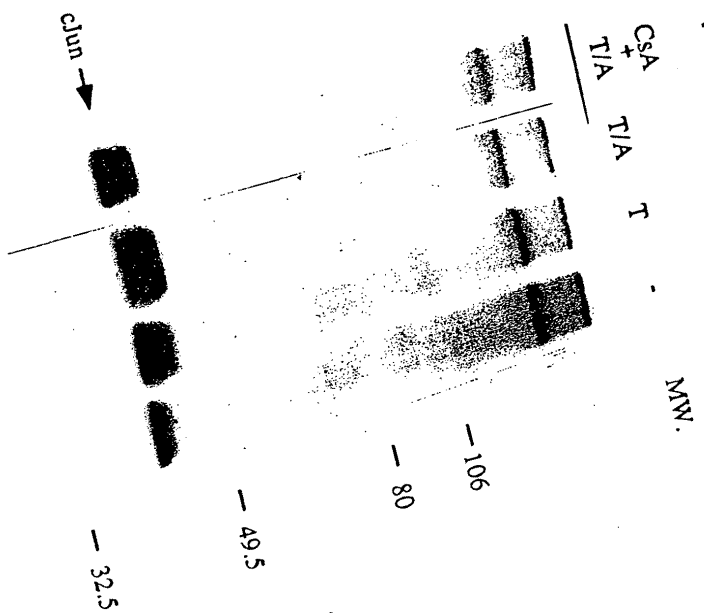
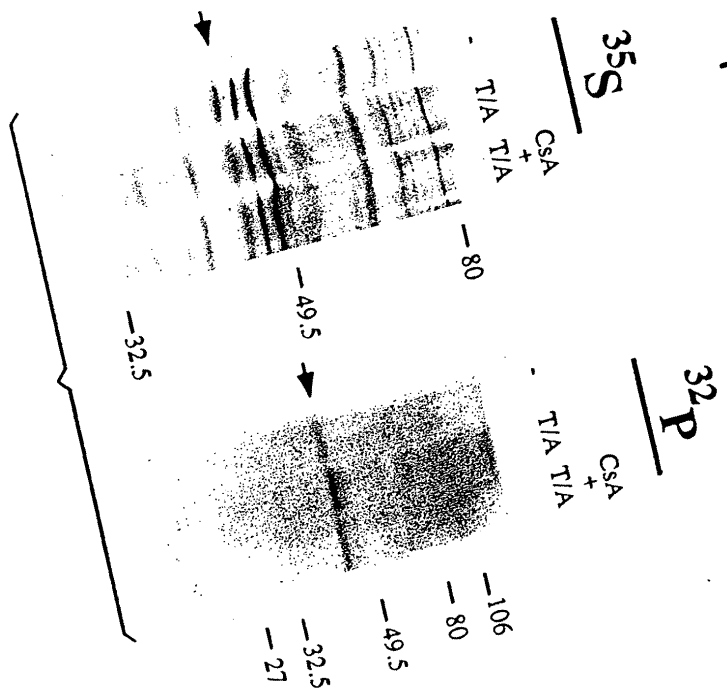


FIG. 12B



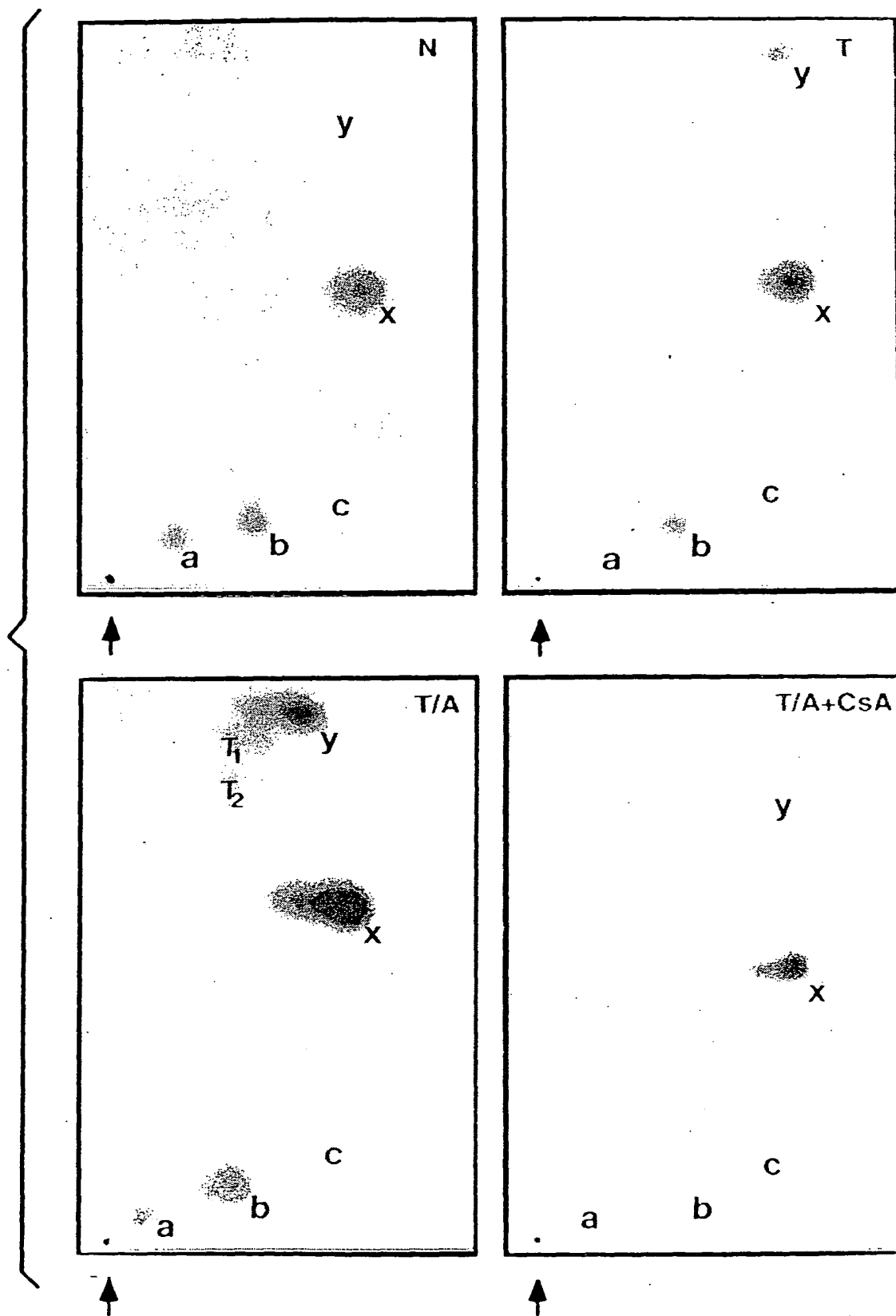


FIG.I2C

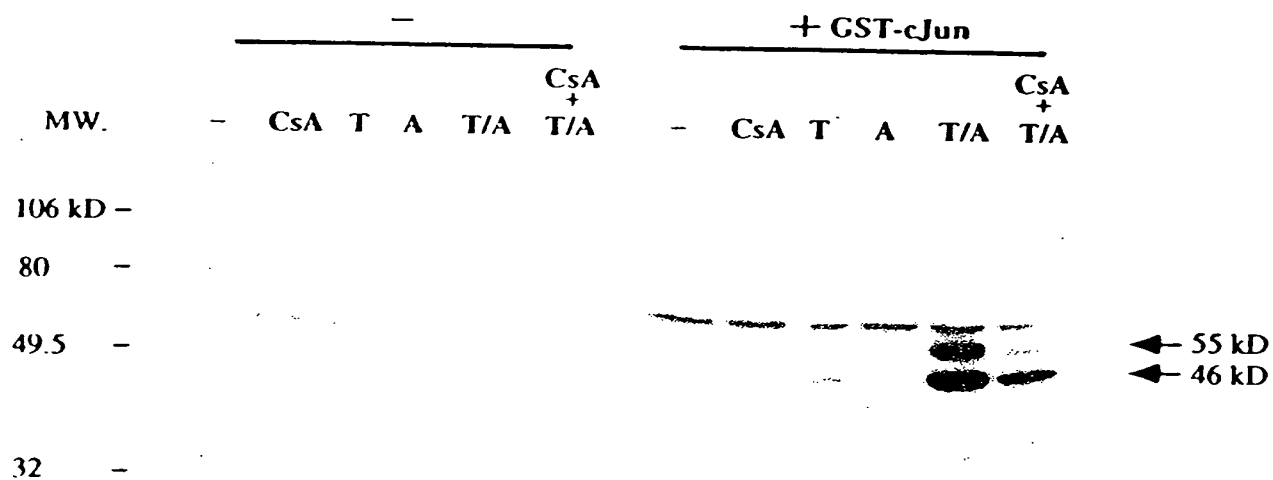


FIG.13A

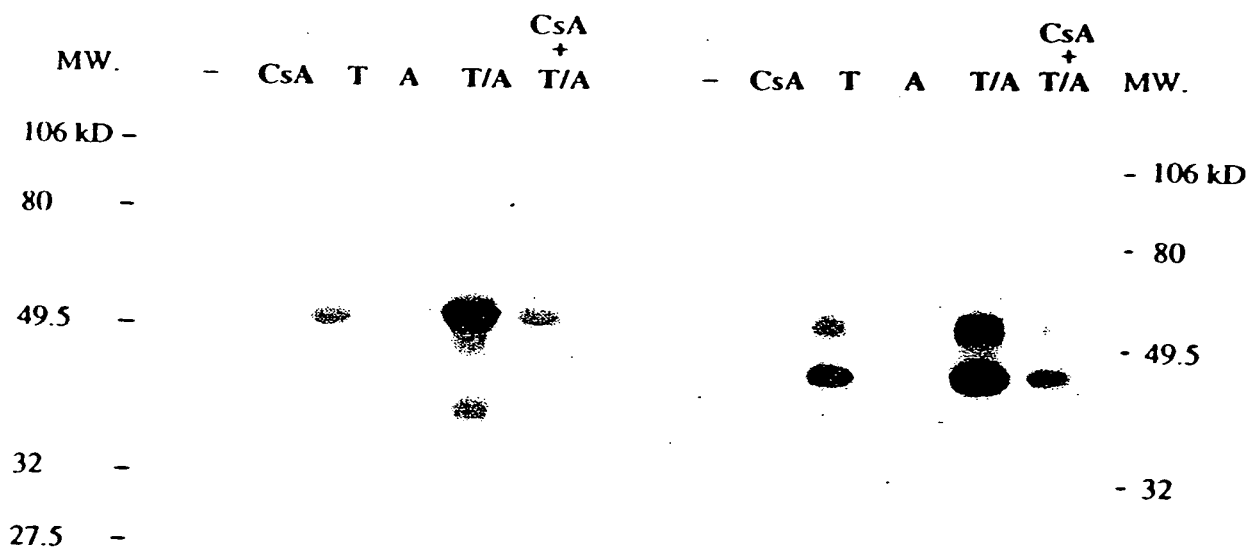


FIG.13B

FIG.13C

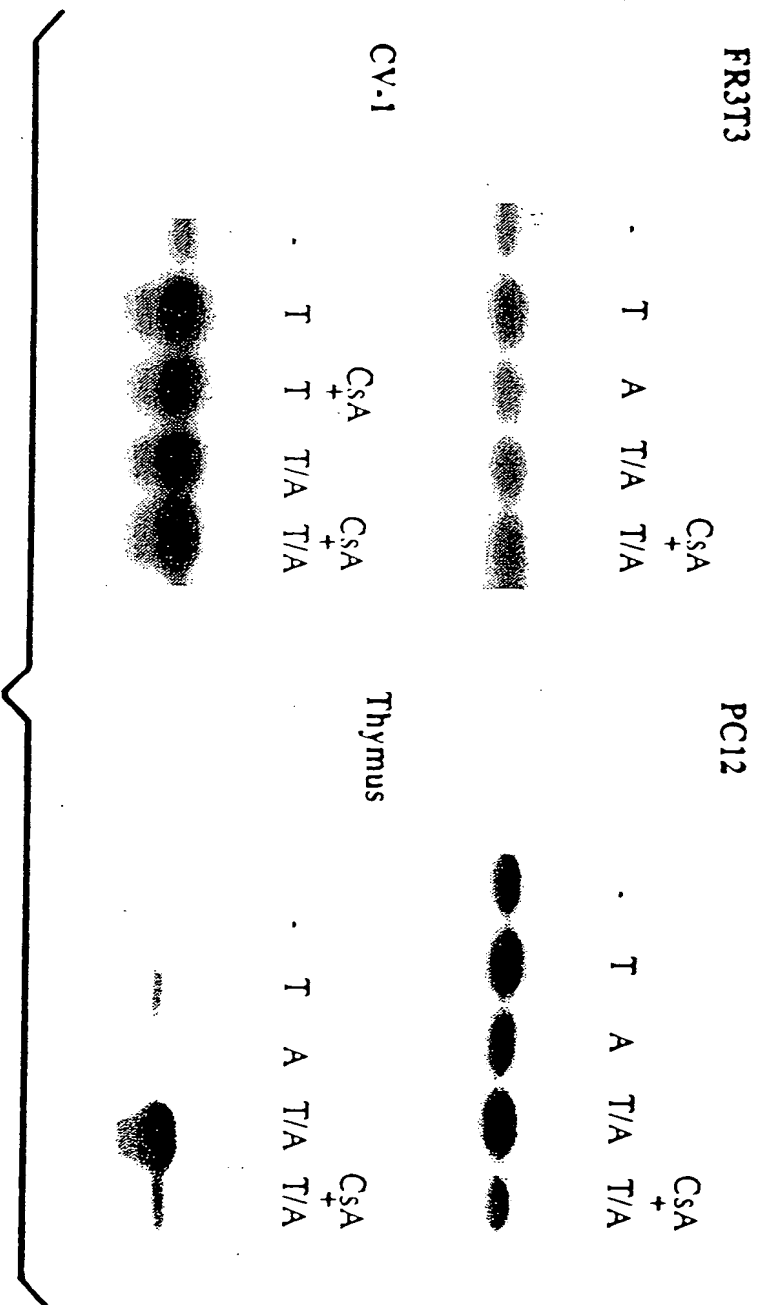
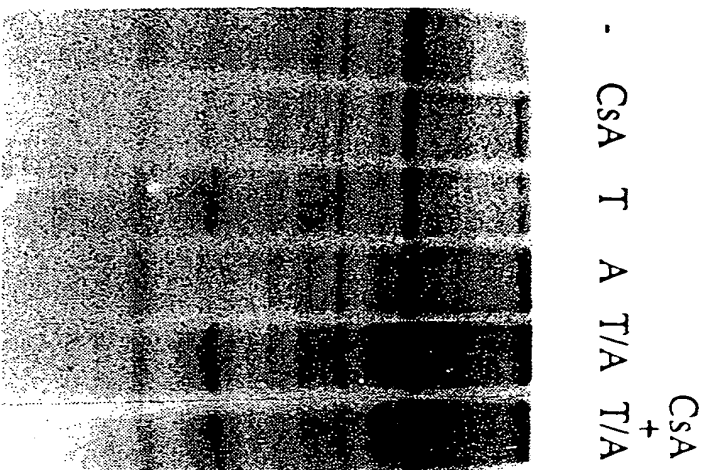


FIG.14

FIG.15A

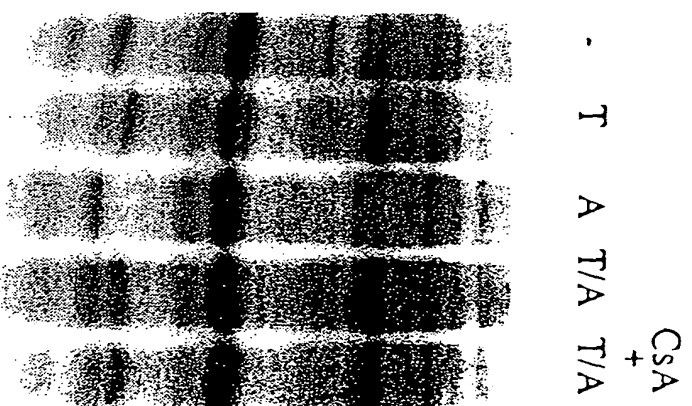


Erk-1 Mut →

- 106
- 80
- 49.5
- 32.5

Erk-1 Mut →

FIG.15C



- 106
- 80
- 49.5
- 32.5

FIG.15B



MBP →

FIG.15D



MBP →

FIG.16A

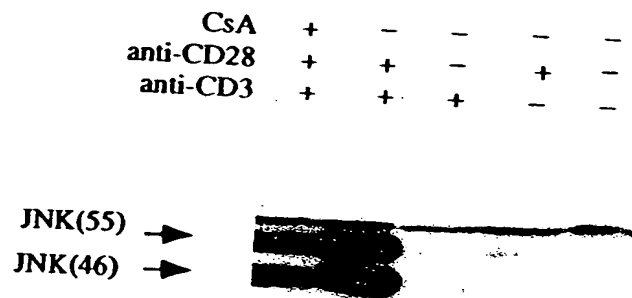


FIG.16B

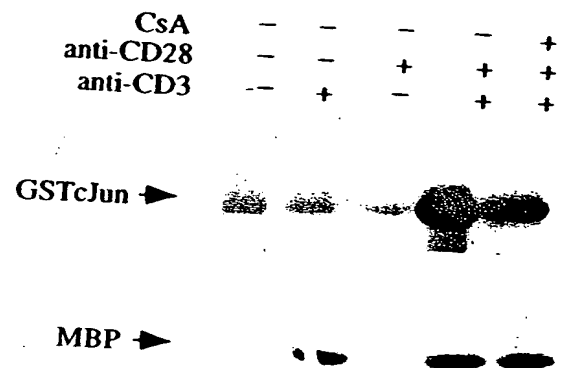
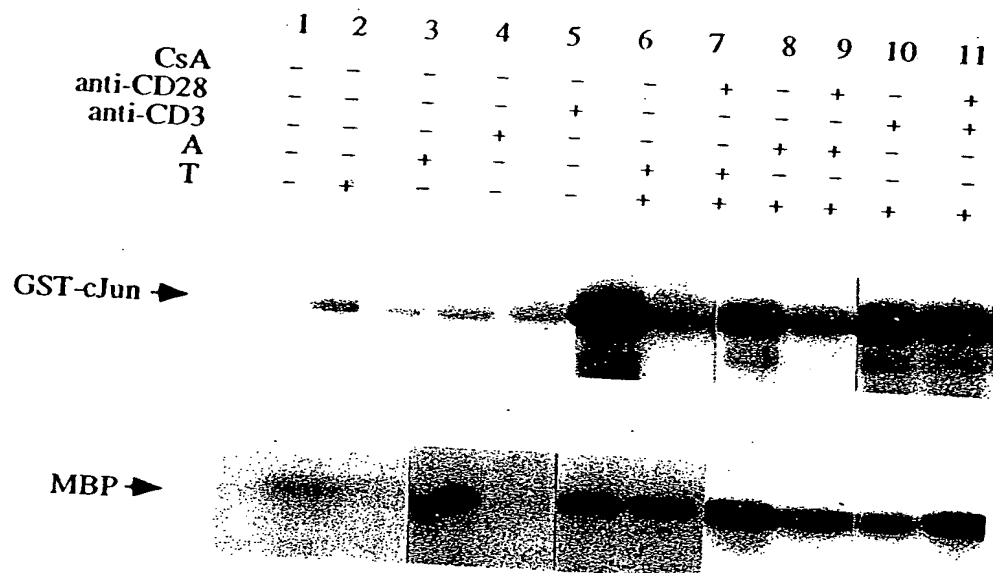


FIG.16C



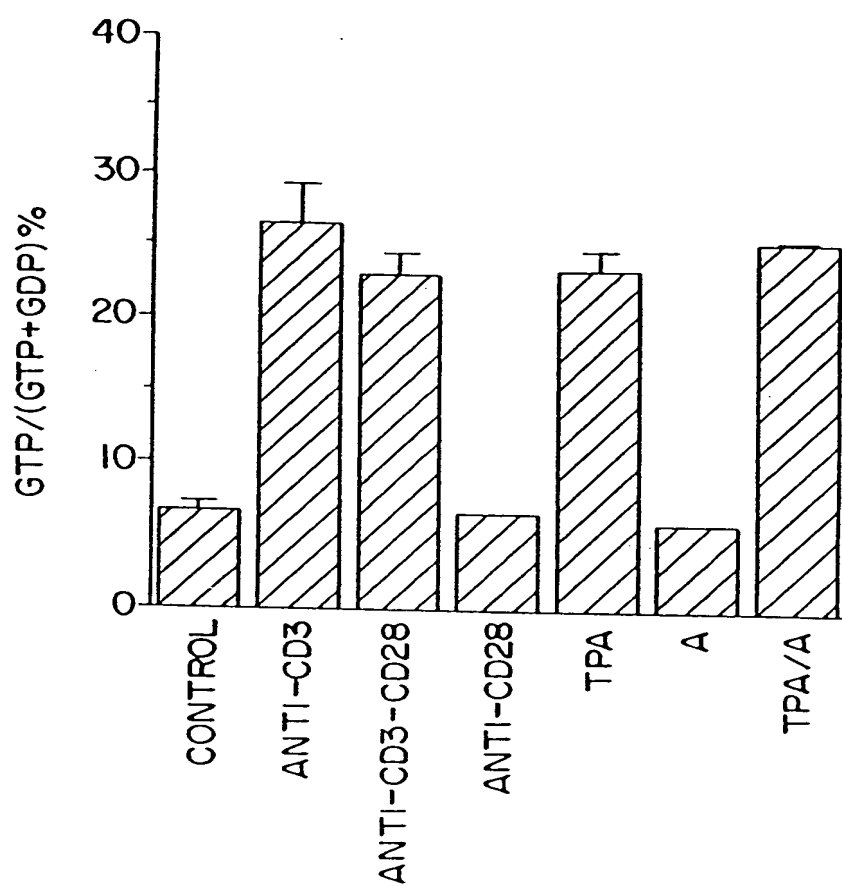


FIG. 17A

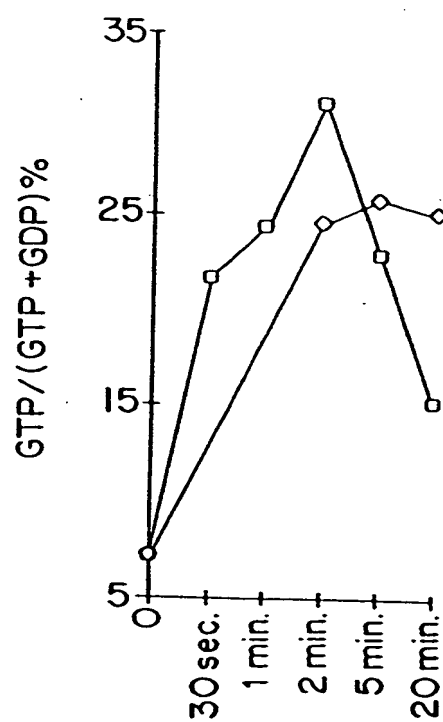


FIG. 17B